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SUGGESTIONS FOR THE STARTING OF NUMERIC EVOLUTION PROCESSES INTENDED TO EVOLVE SYMBIOORGANISMS CAPABLE OF DEVELOPING A LANGUAGE AND TECHNOLOGY OF THEIR OWN

by

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ABSTRACT

This paper is the concluding issue in the series of papers and comments dealing with the functioning of the intelligence mechanisms responsible for biologic evolution. Its aim is to encourage attempts to develop numerical symbioorganisms by artificial evolution processes. The paper suggests only a few examples of modifications one may introduce to the earlier evolution experiments in order to achieve an interaction between the genetic information of the symbioorganisms and the environmental entities (operational elements) on which they are supposed to operate. Such an interaction would imply a conversion of genetic information stored in some kind of genetic language into some form of operation on the environmental entities.

The examples have the only purpose of suggesting a few possibilities. Only by acquiring experience with evolution experiments (for example by repeating earlier successful ones) and attempting thereupon some gradual modifications one may expect to obtain successful results.

1. Introduction

This is the concluding issue in the series of papers and comments dealing with the functioning of the intelligence mechanisms responsible for biologic evolution. The series was initiated in Theoretic Papers Vol.3, 1985, No. 7 and continued in Vol. 4 and Vol. 5. The possibility that other publications on the same subject will follow in the future will depend on the results of the numeric evolution experiments to be proposed in this paper. The experiments we are going to propose are a variation and extention of the experiments presented in the Vol. 3, 1985 paper entitled "Numerical testing of evolution theories. Part I".

In that paper evolution processes of numerical organisms showing a number of properties and evolutionary phenomena in common with biological evolution were presented. A basic phenomenon was, however, missing in the numerical evolution processes obtained, namely the development of a system of communication symbols playing the role of a genetic language.

The development of a genetic language and its implications is a most ambitious goal, involving the development of a high technology by the same kind of evolution process originally used by RNA molecules, and leading to the following developments already mentioned in earlier issues:

The first language and the first technology on Earth was not created by humans. It was created by primordial RNA molecules almost 4 billion years ago.

Is there any possibility that an evolution process with the potentiality of leading to comparable results could be started in the memory of a computing machine and carried on to a stage giving fundamental information on the nature of life? We do not know, but we would like to inquire into the possibilities available.

The first problem we will have to face is: how to modify or replace the reproduction and interaction rules used for the numeric organisms in the preceding evolution experiments (see paper quoted above) in a way liable to promote the development of a genetic language.

The reproduction and interaction rules for the numeric evolution experiments we are going to propose are selected by taking into account the lessons we have learned from our inquiry. Particularly the results presented in our second paper on the origin and evolution of the genetic code (see Theoretic Papers, Vol.4, 1986, No.7, second paper) have been important for the evolution experiments we are going to propose. The main lesson learned from this study is that many of the original properties and functions of RNA molecules are still conserved with surprisingly unconspicuous modifications by modern tRNA, mRNA and rRNA molecules. This suggests that the chemical and physical environment inside the cell and particularly in the cellular nucleus is not drastically changed from the original environment in which the RNA molecules lived when life originated. One of the main functions of the cell and its various components is apparently to maintain an internal environment similar to the environment in which the RNA molecules originated, no matter how drastically the external environment has been changed.

This is an important lesson, because it tells us that no matter how drastically the conditions in the numerical universe may have to be changed in order to promote evolution, the numerical organisms must always have the possibility to change those conditions in a way which will keep their ability to function normally. This condition is essential in order to avoid extinction and allow evolution to proceed uninterrupted. An important portion of the evolution phenomena may have to be responses to potentially harmful environmental changes designed to maintain or restore original conditions or original ability of the numerical organisms to function normally.

2. Selection of reproduction and interaction modes

Before giving detailed descriptions, a few words about the selection of selfreproducing entities to be used will be appropriate. Two main models may seem to be available for a numerical simulation of an evolution process:

(1) An RNA-simulation model, based on a numerical simulation of

the original hypotetic nucleotides and other molecular structures (aminoacids etc.) assumed to have started the evolution process leading to the development of living organisms on Earth.

(2) A numerical symbiogenesis model, based on the same kind of procedures used in earlier numerical evolution experiments (Barricelli, 1962 and 1985).

Besides the obvious difficulties of describing numerically an RNA-simulation model and obtaining the necessary information for this purpose, there are important considerations concerning the aim of the investigation proposed. If the aim of the investigation were a precise description of the way in which terrestrial life forms (or life on Earth) originated, including the chemical aspects of the phenomenon, the RNA-simulation model would be the better alternative assuming it could be realized. But if the aim is to explore the possibilities of general, not necessarily chemical, evolution theories, such as symbiogenesis theory, and identify implications valid irrespective of the nature (chemical or non-chemical) of the organisms involved, then the numerical symbiogenesis model is much to prefer. This model, if compared with the evolution of terrestrial life, will give a clear distinction between the phenomena which are a direct consequence of the evolution theory to be tested (for ex. symbiogenesis theory) and the life processes which are partly or entirely a consequence of chemistry.

Our proposal will be based on a numerical symbiogenesis model which is a modification of the model employed in our earlier evolution experiments. By this choice, the experience obtained in the earlier evolution experiments is expected to be helpful for the planned undertaking.

3. The original numerical symbiogenesis model

We shall start with a brief description of the original numerical symbiogenesis model before presenting the proposed modifications. Our description is an abstract of the reproduction and interaction rules for numbers disposed in a series of squares representing a one-dimensional universe, presented in the

Barricelli 1962 and 1985 paper "Numerical testing of evolution theories. Part I". The main rules are presented in the paper's section 5 and 6, explaining how the numbers in a one-dimensional universe (first line in the figures) are moved and/or reproduced in the subsequent lines (representing subsequent generations) in the respective figures. But before describing these main rules it may be helpful presenting a simpler example of selfreproducing numbers illustrating the concept. For instance, one may use as self-reproducing entities a group of numbers written in the first line of a crossection paper - see fig.1, where negative numbers are underlined - and one may choose arbitrarily a reproduction rule for these numers. The reproduction rule used in fig. 1 is the following: in one time unit (generation) a positive number m is reproduced m squares to the right and a negative number n is reproduced -n squares to the left. The result obtained from the first line by following this reproduction rule is recorded in the second line. Applying the same reproduction rule to the second line, one obtains the third line, etc. Of course, in order to prosecute the operation one would have to establish some rule to decide what to do in the cases in which two different numbers happen to fall (collide) in the same square. This will be done below, by introducing hereditary changes (or mutations).

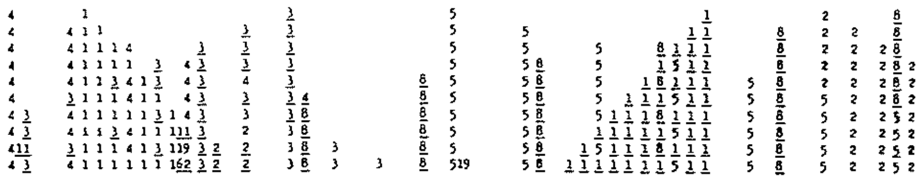


Fig. 1. Selfreproducing numbers (see text). Adaptive selection but no extensive evolution phenomena are possible.

There is no difficulty in defining mathematical entities which besides the faculty to reproduce have the property of undergoing hereditary changes. In the numerical entities defined above, one may for instance choose some mutation rules to apply when two numbers collide in the same square. The number to be put in the collision square may be different from the two colliding numbers and may therefore represent a mutation.

The following mutation rule has been applied in fig. 1: two numbers which collide in a square are added together, and from the result one subtracts the content of the square above the collision square (except when the square above the collision square is empty, in which case nothing will be subtracted). If three numbers collide in the same square, they are added together, and from the result one subtracts twice the content of the square above the collision place, and so on.

In this manner we have created a class of numbers which are able to reproduce and to undergo hereditary changes. The conditions for an evolution process according to the principle of Darwin's theory would appear to be present. The numbers which have the greatest survival in the environment created in fig. 1 by the rules stated above, will survive. The other numbers will be eliminated little by little. A process of adaptation to the environmental conditions, that is, a process of Darwinian evolution, will take place.

This process does not, however, fulfil the requirements for a meaningful evolution experiment (see criticism in section 2, Barricelli 1962 and 1985). In order to fulfil such requirements (see section 3 and 4, same paper), we must introduce reproduction rules which require some cooperation (symbiosis) between the reproducing numbers. These rules are presented below

a) A number n will be repeated n squares to the right (if positive) or -n squares to the left (if negative) in the next row (see fig. 2 and 3). This operation will be called "translation to square (n) of next row without reproduction".

b) If the new position (n) happens to be below a square occupied by a different number m then a second n will be placed in position (m), which means m squares to the right (if m is positive) or -m squares to the left (if m is negative) of the original n, but in the next row. This way a number n can reproduce if another number m different from n is present (see fig. 4).

If in this process the number n happens to come several times below different numbers it may reproduce several times (see fig. 5, where the number 4 from the second row appears 3 times in the third row).

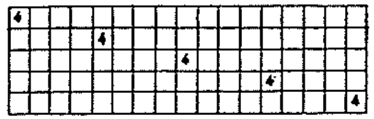


Fig. 2.

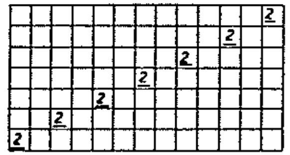


Fig. 3.

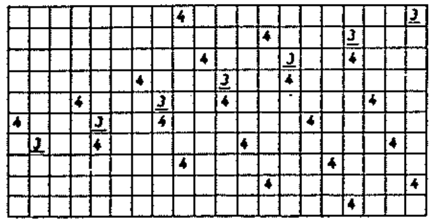


Fig. 4.

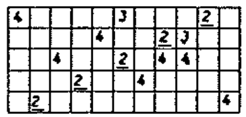


Fig. 5.

Fig. 2,3,4,5. Reproduction rules requiring symbiosis (see text).

The above reproduction rules are made with the purpose of permitting reproduction only when a numerical entity is together with other entities different from itself. A symbiotic cooperation between different numerical entities is thereby rendered necessary for reproduction.

To the above reproduction rules one may add arbitrary mutation rules, for instance by taking advantage of the cases in which two different numbers collide in the same square. To begin with, a rule will be used in which no mutation can occur. The square in which two different numbers collide will be left empty, only marked by a cross (X) or "collision sign". If two identical numbers collide, one of them remains in the collision square.

In fig. 6. the absence of mutations is clearly manifested by the fact that the original numbers 5, 1 and -3 are present everywhere and no new number appears. However, in a few generations the numbers organize themselves into a stable configuration (5, -3, 1, -3, 0, -3, 1, 0 where an 0 marks an empty square) which is present everywhere in the figure. This kind of stable configurations will be called "numerical symbioorganisms". In the rest of this paper it will be shown that symbioorganisms have many properties similar to those observed in living structures. Some of the life-like properties of symbioorganisms which will be present below are termed:

(A) Selfreproduction; (B) Crossing; (C) Great variability; (D) Mutation (if the rules stated above are changed in order to permit mutation); (E) Spontaneous formation; (F) Parasitism; (G) Repairing mechanisms; (H) Evolution.

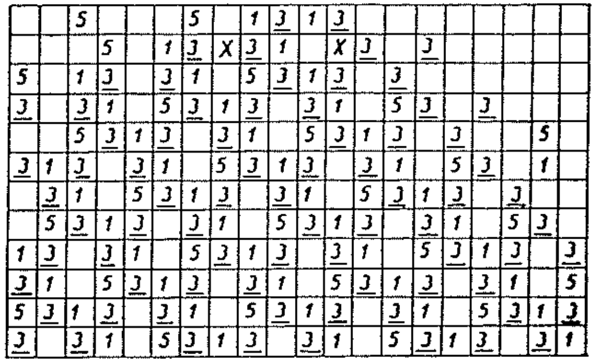


Fig. 6.

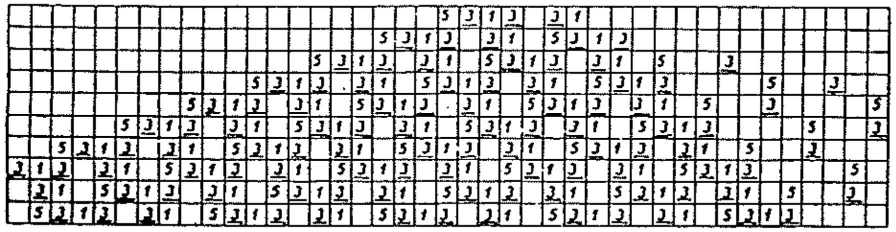


Fig. 7.

Fig. 6 and 7. Formation of a symbioorganism (6) and its reproduction characteristics (7).

4. General properties of symbioorganisms

Symbioorganisms do not have to be of numerical nature. Any elements with the property of self-reproduction and symbiotic cooperation may associate into symbioorganisms of some sort, no matter whether they are of numerical, chemical, or any other nature. According to the symbiogenesis theory, living organisms are the particular kind of symbioorganisms which arise when organic molecules are used as self-reproducing elements.

Some general properties which one may expect to find very often in sÿbioorganisms and all of which are to be found in numerical symbioorganisms are the following:

A) Selfreproduction. In fig. 7 it is shown that the symbioorganism (5, -3, 1, -3, 0, -3, 1, 0) - which arose in fig. 6 is able to reproduce itself.

B) Crossing. In fig. 8 and 9 the two symbioorganisms (9, -11, 1, -7) and (5, -11, 1, -3) are crossed. The second parent organism differs from the first one by two heredity characters, 5 instead of 9 and -3 instead of -7. In fig. 8, where the first organism was placed to the left, the second to the rigth, the crossing product obtained was the recombinant (5, -11, 1, -7). In fig. 9 on the contrary, where the order of the two parent organisms was reversed, the complementary recombinant (9, -11, 1, -3) was obtained. If these two crossing products are crossed with one another, one can obtain again the parental structures of the previous crosses as shown in fig. 10 and 11. Not all symbioorganisms do cross as neatly as these. Often one or two of the crossing products are not competetive in the presence of the parent organisms and can simply not arise, nor could they survive if they did. Nevertheless, the very existence of so simple a solution of the crossing problem is of great theoretical significance.

C) Great variability. Each symbioorganism may consist of any number of elements (genes or numbers) and each element may have several allelic states. The number of varieties which can arise is practically unlimited. This does not mean that every symbioorganism, no matter how primitive will show a

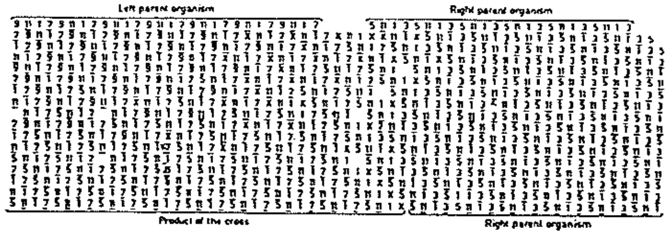


Fig. 8.

Fig. 9.

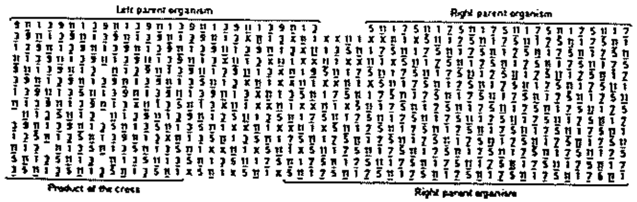


Fig. 10.

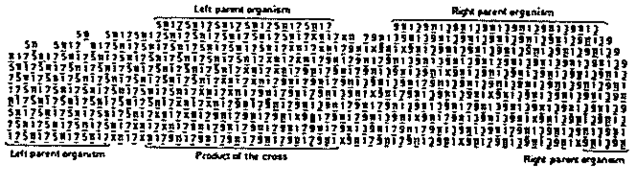


Fig. 11.

Fig. 8. 9. 10, 11. Crossbreeding in numeric symbioorganisms (see text). Crossing rules similar to those of haploid organisms.

great variability. But under proper conditions many symbioorganisms will (see Barricelli 1962 and 1985, fig. 24, generations 600, 1000, 1200, 1300, 1400, 1500, 1600, 1700 and 1800).

D) Mutation. To obtain mutations it is sufficient to change the rules for collision of different numerical elements. The change will have to be rather gentle if one wishes to keep the properties listed above.

All mutation rules which will be used in this paper consist in replacing some of the collision signs X (marking squares in which two different numbers have collided) by a new number or mutation.

One example of such mutation rules is the following (Rule A):

1) An X (collision sign) which happens to be under an occupied square remains.
2) An X which happens to be under an empty square or under another X is replaced by a number M (mutation) whose absolute value is equal to the distance between the closest number to the left and the closest number to the right of the empty square in question (the distance is measured in number of squares). If the two numbers have the same sign, the mutation M will be the positive distance (sign +); if the two numbers have different signs, the mutation M will be taken equal to the negative distance (sign -).
3) If there is no number to the right or to the left of the empty square above the X (collision close to a border of figure) the X remains.

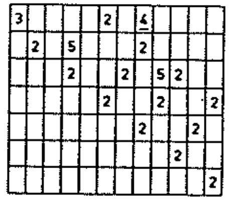


Fig. 12.

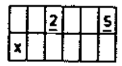


Fig. 13.

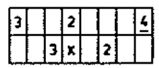


Fig. 14.

Fig. 12,13,14. The A-mutation rule.

For instance, in fig. 12 at the second line where the two numbers 3 and -4 collide, one finds +5 instead of an X because the distance between the closest number to the right and the closest number to the left in the line above is 5 squares and because they have the same sign (both are positive). On the other hand in fig. 13 the place where the two numbers -2 and -5 collide is marked with an X because there is no number to the left of X in the line above. Likewise in fig. 14 the X remains where the two numbers 3 and -4 collide since the square above the collision place is not empty.

Several other mutation rules which have been used in evolution experiments will be defined in this paper. Although the mutation rule may influence the kind of symbioorganisms which arise, the general character of the phenomena remains the same.

E) Spontaneous formation. In fig. 15 the first row contains only the numbers 1, -1, or empty squares selected by a random procedure (heads and tails was played with two coins; two heads indicate 1, two tails -1, one head and one tail indicates an empty square). In the following generations other numbers than 1 and -1 arose by mutation and various organisms recorded in the figures 16, 17, 18, 19, 20, 21, and 22 were formed.

This experiment shows that under favourable conditions symbioorganisms can be formed quite frequently and the formation of a symbioorganism is not a rare event. But of course if the environment is modified by the presence of other symbioorganisms such spontaneous formation can be prevented.

F) Parasitism. One may note that one of the symbioorganisms (1, -2, 1, 1, -2, 0) a so called tregener which arose near the upper right border of fig. 15 in the above experiment (the one which is recorded in fig. 17) does not reproduce completely. In fig. 17 the symbioorganism loses its elements one by one and at the end nothing remains. However, if the same symbioorganism is sowed together with the symbioorganism (1, -1) which acts as its host it will reproduce normally as shown in fig. 18. At the same time, the host is destroyed little by little. This relationship between two symbioorganisms is very similar to the phenomenon which in biology is called parasitism. The same terminology may be used here. The symbioorganism (1, -2, 1, 1, -2, 0) shall be called a parasite of (1, -1).

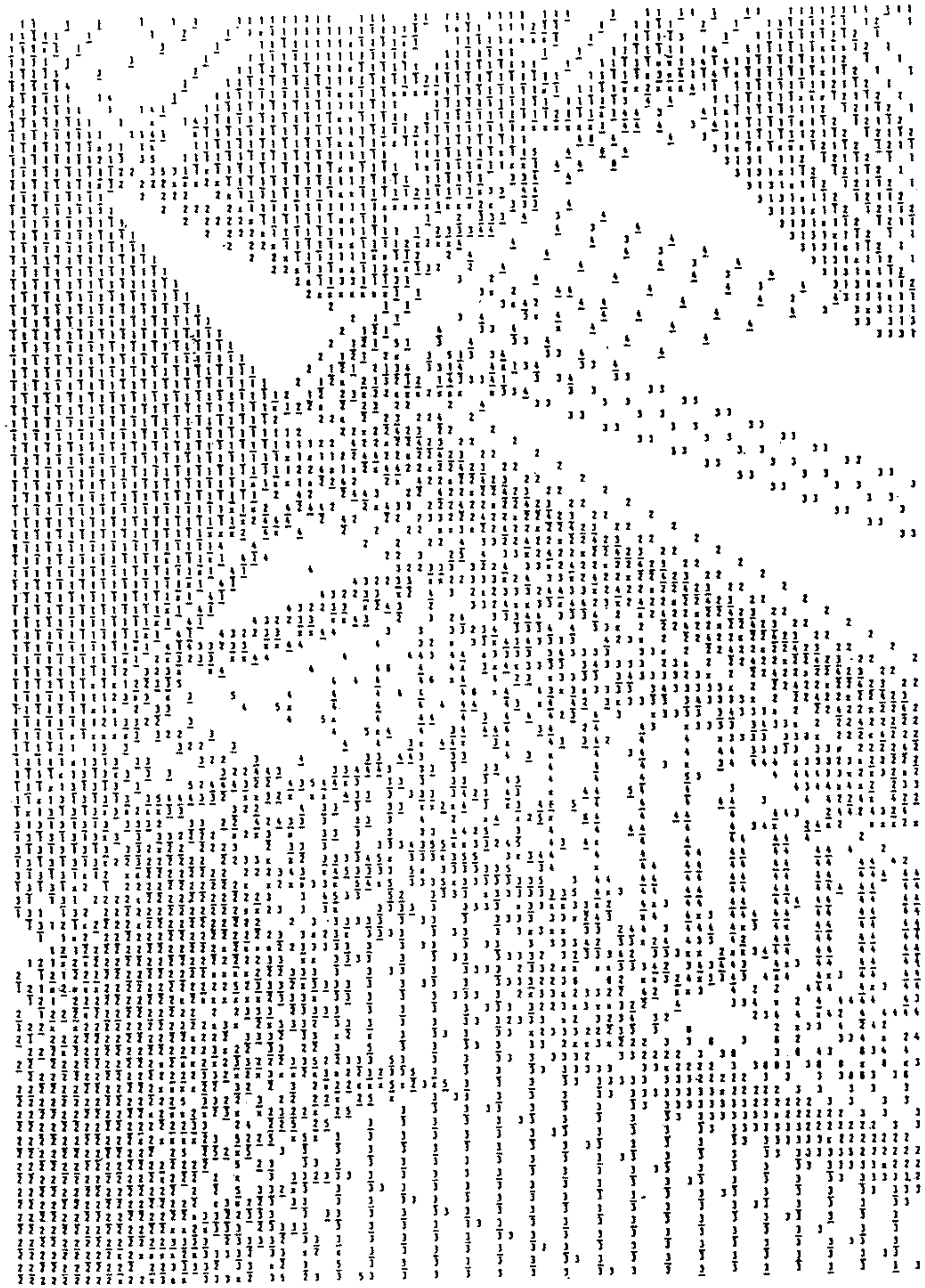


Fig. 15. Spontaneous formation of symbioorganisms in an experiment started with random numbers

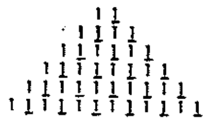


Fig. 16

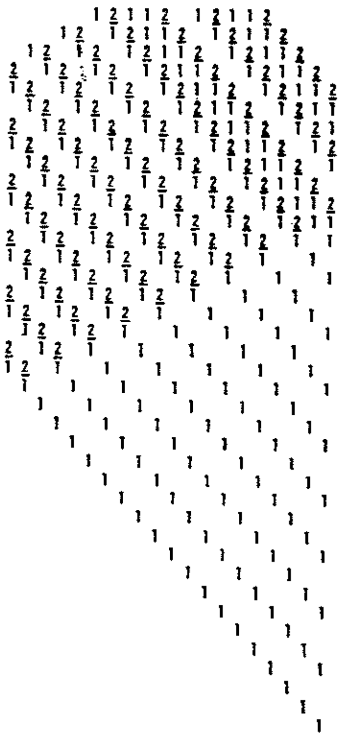


Fig. 17

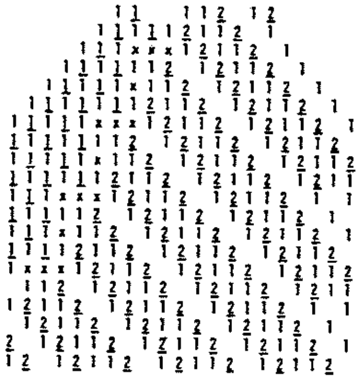


Fig. 18

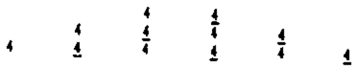


Fig. 19

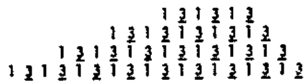


Fig. 20

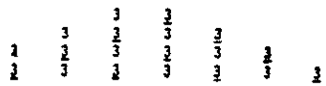


Fig. 21

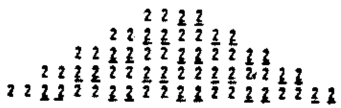


Fig. 22

Fig. 16,17,18,19,20,21,22. Reproduction of symbioorganisms which arose in the experiment of fig. 15. One organism (parasite Fig.17) does not reproduce succesfully when alone. However in association with its host organism (Fig. 18) it reproduces normally.

Parasitism is a very common phenomenon among symbioorganisms and it constitutes one of the major difficulties in the performance of numerical evolution experiments. Often an evolution process will end with the destruction of the species by a parasite which also will die out once the host is destroyed.

G) Repairing mechanism. Damages are usually repaired by cooperation among several neighboring symbioorganisms. The repairing process may often be partially or completely successful even if all the symbioorganisms present are damaged by removing (cancelling) some of their genes. In this case the repairing is more likely to succeed the greater the number of symbioorganisms cooperating.

This phenomenon presents a startling analogy with the repairing mechanism known in bacterial viruses as "reactivation by multiple infection with inactivated (for ex. irradiated) phages".

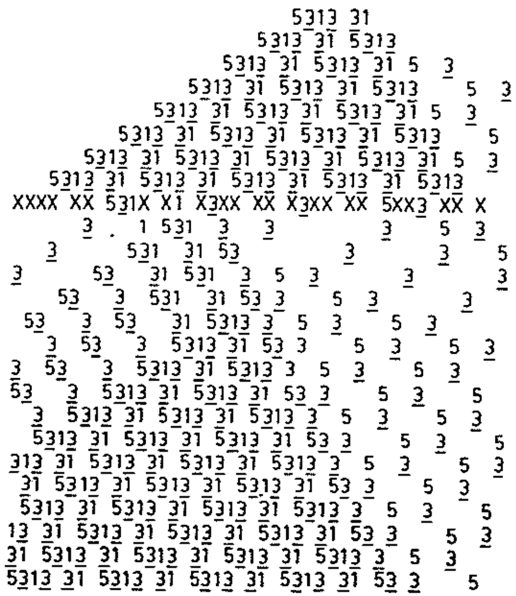


Fig. 23. Repairing mechanism by cooperation of several seriously damaged symbioorganisms. Removed numbers (damages) in the ninth line are marked by X's.

In all the 5 odd symbioorganisms of line 9 in fig. 23, a large fraction of the numerical elements, selected by a random procedure, are cancelled (replaced by an X in the fig.). The damaged symbioorganisms left reconstitute the original pattern in a few generations. None of the 5 odd damaged symbioorganisms of line 9 would in itself have been able either to reconstitute the original pattern or else to generate another pattern able to survive and reproduce.

Recovery by the above repairing mechanism is not always complete, and the reconstituted symbioorganism may often show deficiencies (missing genes). A deficiency is not always lethal, and the symbioorganism may therefore survive as a mutant.

H) Evolution. In fig. 15 the only example of hereditary change in a symbioorganism is the change which transformed (1, -1) into (1, -3) at the left side of the figure around generation 60. This change was induced by an external element (-3) entering the symbioorganism. Using high speed computers, evolution experiments have been performed which involved a large number of hereditary changes. Some of these evolution experiments are described in the quoted paper. The result of such experiments can be summarized as follows:

Symbioorganisms can be completely modified. Their complexity may drastically increase, and they can branch into different species which are unable to interbreed.

The evolution leads to a better adaptation to the artificial environmental conditions and a greater ability to compete with other symbioorganisms (see competition tests, Section 9, Barricelli 1962 and 1985). Both mutation and crossing phenomena played a central part in evolution. To begin with, most of the crossing was performed by single elements (genes) which left one symbioorganism and entered another symbioorganism. Later the "regular" crossing mechanism described in fig. 8, 9, 10, and 11 became predominant. Such regular crossing is very similar to the crossing in haploid species of living organisms.

The results of evolution experiments lasting for more than 5000 generations and leading to complex symbioorganisms with 72 genes (numbers) are described in the Barricelli 1962 and 1985 paper in the sections 7, 8, 9, 10, 11 and 12. The experience obtained in these evolution experiments can be useful for the present research program.

5. Comparison with RNA evolution

Our next step will be to establish some term of comparison between the described numeric evolution processes obtained and the hypothetical RNA evolution phenomena described in the second paper on the origin and evolution of the genetic language (Barricelli 1979 and 1986).

Apparently the only meaningful way of attempting a comparison can be based on the amount of information involved in the respective survival strategies of the two kinds of symbioorganisms as measured by their respective hereditary (or genetic) information. That is what we may call the information-theoretical base of comparison, a standard method of comparing the complexities of different machines.

We may start by comparing the hereditary information of numeric symbioorganisms with that of primordial RNA organisms at the stage when they started collecting aminoacids and possibly other molecular structures leading to the origin of the first collector languages, which eventually evolved into modern genetic languages.

Modern tRNA molecules are believed to have inherited their role, and perhaps even some of their genetic information, from the RNA molecules which provided for the collection of aminoacids in the primordial collector societies of RNA molecules (Barricelli 1979 and 1986). The hereditary information of the primordial collector RNA molecules can only very roughly be evaluated by looking at the number of nucleotides in modern tRNA molecules, all of which have between 60 and 100 nucleotide bases and considerable structural similarities suggesting a common origin, or a parallel evolution. With the modern 4-letter genetic alphabet this would imply between 120 and 200 bits (2 bits per nucleotide) of information; or actually more, because most tRNA contain a few unusual (altered) bases thus requiring some extra information in order to program the nucleotide alterations. In the original 2- letter genetic alphabet (one bit per base) it would imply scarcely 100 bits per RNA, assuming the number of nucleotides was about the same. If base analogue substitutions were frequent (see Barricelli 1979 and 1986) we may operate with an estimated amount of information between 100 and 200 bits per RNA molecule in the primordial collector societies.

Let us now look at the amount of information in the numerical symbioorganisms developed in our evolution experiments. The most complex symbioorganisms which were developed at the end of our evolution experiments consisted of 72 numbers (or numerical elements), each one replaceable by other numbers as a result of crossing and/or mutation (just as RNA bases are replaceable by other nucleotides). The number of possible replacements for each numerical element was restricted by the structural properties of the respective numerical organisms, but was in most cases larger than 2. In other words each numerical element carried an information larger than one bit, and each numeric symbioorganism carried an information comparable to (and possibly sufficient to identify) the nucleotides of a primordial tRNA modelcule.

The numerical symbioorganisms did not have any gadgets to play with, such as the aminoacids and other molecular structures carried around or collected by primordial RNA molecules in order to improve their survival possibilities. We are going to give them some gadgets they can work with.

6. The introduction of operational elements

Items (or gadgets) not carrying genetic information, but moved around or modified by symbioorganisms in their survival strategy operations (such as the aminoacids and other molecular structures manipulated by primordial RNA) are designated as "operational elements". We shall first describe some of the original functions of the operational elements used by primordial RNA molecules before venturing any suggestion about the operational elements one may supply to the numerical symbioorganisms.

Recent discoveries have established that RNA molecules are capable of performing quite a few operations, necessary for their reproduction and survival, which were earlier considered an exclusive domain of protein activity (Gilbert 1986, Westheimer 1986, Lewin 1986). These discoveries strongly support the notion that primordial RNA was able to carry out all the operations necessary for its reproduction and survival in its original environment without assistance from proteins or any other operational elements (just as well as the numeric symbioorganisms are). What introduced the need for operational elements, like aminoacids and proteins? We may venture an answer to this question. Primordial RNA had originally no way of producing nucleotides. No matter how abundant the nucleotides might have been in the original environment the rapid (geometrical) growth of RNA molecules would eventually put an end to the nucleotide supply. Shortly speaking, the environment was rapidly deteriorating. The nucleotide supply was not necessarily the only cause, but certainly an important cause of the deterioration. What could be done in order to avoid such deterioration?

Evidently primordial RNA must have originated in an environment in which nucleotides were available and must therefore have been formed by a natural process not involving living organisms. We do not know what kind of process that was. But it is an easy guess that aminoacids and polypeptides (or primitive proteins) may have been involved. The transportation of crucial aminoacids and possibly other molecular ingredients in the places where nucleotides were being formed could greatly have accelerated the nucleotide formation process. This seems to be the best guess about the way in which the transportation of aminoacids, the first operational elements, was adopted by RNA molecules. From then on the use of operational elements has become a basic feature in the survival strategy, and the original skills of RNA molecules have largely been supplemented or replaced by protein activity, under genetic control.

The very existence of a genetic control of operational elements implies the translation of a system of genetic signals (or language) into a system of operations on the operational elements. This applies for the RNA molecules as well as for the numerical symbioorganisms. Let us consider some examples of operational elements one may introduce and submit to the genetic control of numeric symbioorganisms.

7. Suggestions for an attempt to introduce operational elements genetically controlled by numerical symbioorganisms

We shall present a few tentative suggestions for the introduction of operational elements to be modified and gradually adapted by the programmer attempting an evolution experiment.

The only way which has been successful so far in the development of long-lasting numerical evolution processes by computer machines has been based on trial and error procedures in which the programmer has been allowed to introduce tentative modifications in the operational setup. In the earlier described evolution experiments the modifications were restricted to changes of mutation rules in some parts of the life space (universe). We are going to include several other properties of the symbioorganisms and their life space. One main purpose is giving to the programmer some freedom of choice thus opening a possibility to influence and direct the evolution process.

The main function of the operational elements we are going to propose is: giving to the numeric symbioorganisms a possibility to mend deteriorating environmental conditions thus restoring a situation favourable for their survival and reproduction (the same philosophy which is supposedly behind the early evolution of primordial RNA). This also implies the introduction of environmental conditions which can deteriorate or improve under the influence of factors which can be controlled by the symbioorganisms.

A few specific assumptions with the main purpose of simplifying the presentation of the subject (even though they are not strictly required and can easily be replaced with other assumtions which may have a similar purpose) are the following:

1. We assume we are using a computing machine with 48 bit words. We select a series of N words (or memory positions) to represent the numbers (elements), such as the numbers in the figures 2,3,4,...,23, of which the numerical organisms are composed, and any additional information we may need about each number. N will be called "the size (or life space) of the numerical universe".

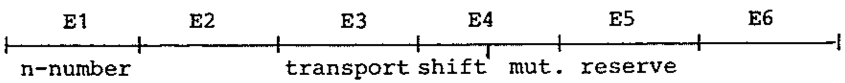
2. Each word (element) of the universe is supposed to be subdivided into 6 segments of 8 bits each, designated as E1,E2,...,E6, see fig. 1A.

Fig. 1A. First example. Original approach

3. Each segment can be further subdivided whenever needed, for example into an upper and a lower segment of 4 bits each. In fig. 1A the E4 segment is, for example, subdivided into a lower E4, and an upper E4 assigned to the identification of mutation rule.
4. In fig. 1A the first segment E1 is supposed to contain anyone of the numerical elements (n-numbers) used in the figures 2,3,...,23. Positive n-numbers are the ones which contain 0 in the first bit. Negative ones contain 1 in the first bit. Only n-numbers between -63 and +63 are allowed.
5. In the fig. 1A only the n-number and the local mutation rule (number in the upper E4, mut.) are identified. This kind of arrangement can be used in order to repeat the same kind of evolution experiment described before, and does not introduce any new possibilities.

If we want to introduce some new features in our evolution experiments we may assign various functions to some of the other segments E2,E3, etc. This is done in the second example presented in fig. 2A.

Fig. 2A. Second example.



Explanations:

n-number: Same as in fig. 1A (is moved and reproduces like the numbers in fig. 2,...,23).

mut.: Same as in fig. 1A (is not moved).

reserve: Every new n-number produced in this place (either by reproduction or by mutation) is added to the reserve, except if the resulting sum becomes larger than 63 or smaller than -63, in which case the n-number is replaced by 0 and the reserve remains unchanged.

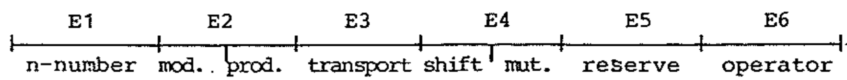
transport and shift: If shift contains 0, then transport and reserve are not interchanged. If shift contains 1, then transport and reserve are interchanged before the n-number is moved. Transport is moved (but not reproduced) together with the n-number, provided the transport place it is supposed to move into is empty (=0). The programmer is free to choose other possibilities for the cases in which shift contains a number greater than 1 (use your imagination). The choice opportunities may allow directing evolution in the ways desired, just as the choice of mutation rules successfully used in earlier evolution experiments.

The reserve introduces a boundary to reproduction, which can be inhibited when the reserve exceeds ±63. But the transport opportunities give the possibility to move cumbersome reserves away and replace them by better ones. By these and other ways the symbioorganisms may have various opportunities to avoid the effects of a deteriorating competitive environment. Moreover, reserves which are harmful for some symbioorganisms can be harmless or even useful for others, thus opening some new symbiosis possibilities.

Only by starting various evolution experiments, and assessing the problems and difficulties which arise as well as introducing modifications in order to eliminate those difficulties it is possible to obtain satisfactory evolution processes.

A more complex example involving a larger number of operational elements is presented in fig. 3A

Fig. 3A. Third example



Explanations

n-number: Same as in fig. 1 and 2.

mod. is a 4 bit number that can be used in order to modify the operations but not the contents of prod., shift. etc.

prod. At the start it contains the number 7. Whenever the n-number reproduces, 1 is subtracted from the prod. of the reproducing n-number and added to the prod. in the position where the number reproduces. If the sum is greater than 7 the result will be reduced to 7. The n-number cannot reproduce if the contents of prod. is zero.

transport and shift. Same as second example in the cases in which shift contains 0 or 1. In case shift contains 2, transport and operator are interchanged. In case shift contains 3, the contents of transport is replaced by 0. By using shift values >3 one may find ways to modify shift values by using operator and/or other operational elements (transport and shift are moved but not reproduced together with the n-number).

mut. Same as in examples 1 and 2 if mut. contains one of the four numbers 0,1,2,3. Other mut.-values (contents) can be used in order to increase the contents of prod. by 1 or more thus creating a position in which the contents of prod. can be increased (mut. is not moved).

reserve. Same as in example 2.

operator. Can be used in order to modify at will the effects (but not the contents) of other operational elements in the same word (or memory position).

Concerning the movement and reproduction of the operational elements we suggest the following rules which may be modified if needed during the progress of the experiment. The contents of mod. and prod. are moved and reproduces together with the n-number. In case of collision with a different local mod. or prod. number the incoming or reproduced number is substituted for the original local one. The contents of transport and shift are moved (but not reproduced) together with the n-number. In case of collision with a different local number, the incoming number is substituted for the original local one. The contents of mut., reserve and operator are not moved nor reproduced. Only by interchanges with transport (see above) can the contents of reserve and operator be changed.

The sum of all prod. numbers (or prod. supply) is a limited resource which is gradually used up as the n-numbers reproduce, because the prod. number of the progeny is subtracted from the prod. number of the parent (see above). Reproduction stops when prod.=0. Only by creating positions (see mut.) in which prod. is locally incremented can an adequate prod. supply be maintained. The prod. supply may play a role similar to that of other limited energy of food supply resources in terrestrial life.

8. How to start an evolution experiment

The only way we know of, which can lead to successful evolution processes is the trial and error approach used in the preceding evolution experiments (Barricelli 1962 and 1985). We suggest that an experiment be started by using the rules presented in the first example (fig. 1A). These rules are equivalent to those applied in the earlier evolution experiments and may lead to evolution processes similar to those obtained earlier. At various stages in the evolution process one may attempt to introduce some of the operational elements presented in the second example (fig. 2A). If an attempt is successful one may gradually introduce more operational elements from the second and third example (fig. 3A) discarding unsuccessful attempts as they arise. The programmer will feel free to modify and improve the suggestions presented in the second and third examples as the experiment proceeds. The same or probably more substantial progress in the fitness of the symbioorganisms can be expected in these experiments compared with the earlier ones. The progress of fitness in the earlier experiments was tested by competition tests like the ones described in section 9 and fig. 25 of the Barricelli 1962 and 1985 paper. The same kind of competition tests can be repeated in other evolution experiments.

In any successful experiment each symbioorganism will develop its own competition and survival strategy, as they have done in the past experiments. But if a large number of operational elements important for survival are used, much of the genetic information of the numerical symbioorganisms will be information identifying the operational elements. This information will be contained in a system of symbols (or language) specifying the operational elements and their organization. Instead of working and fighting with their own numerical genes as in the earlier experiments (and in the original RNA molecules which largely operated by using their own polynucleotide molecules, see above) they will operate by using coded genetic messages specifying the operational elements and their organization. The messages will be expressed in a genetic language expected to be developed by evolution together with the symbioorganisms.

It is difficult to anticipate the characteristics of such a genetic language and it may not be easy to identify it whenever it develops (nor is it supposed to be).

It is, however, important to keep in mind that the evolutionary mechanism of a symbioorganisms is a powerful intelligence mechanism (or genetic brain) that, in many ways, can be comparable or superior to the human brain as far as the ability of solving problems is concerned (Barricelli 1963 and 1985). What exactly can be learned by following the evolution of symbioorganisms, their languages and genetic messages is difficult to anticipate. Whether there are ways to communicate with genetic brains of different symbioorganisms, for example by using their own genetic language, is a question only the future can answer. But the study of symbiogenetic evolution processes certainly can be one of the most exciting research objects existing today.

One of the earlier attempts (Fogel, Owens and Walsh, 1966) to solve problems and develop artificial intelligence by evolution phenomena is based on the use of so called automs. An autom is a mechanical or numerical device which upon receiving an input or stimulus (for ex. a number I) responds by producing an output (for ex. a number A) and converting from its present state (designated for ex. by a letter S_1) to a new state (S_2). The autom's response depends on its present state (S_1) and on the input (I) received. The ability of automs to learn a given task (such as

delivering a given series of responses upon receiving a given series of stimuli) is described by Fogel, Owens and Walsh (1966).

We call attention to the fact that each numerical gene of a symbioorganism fulfills the definition of an autom, because it responds to specific stimuli (or inputs) from other numerical genes by producing certain responses and occasionally by changing its state (mutation).

The symbioorganisms we are studying are therefore symbiotic associations of a particular type of automs. The introduction of operational elements greatly increases the variety of automs which can be used in the evolution experiments.

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